

SEQUENCE LISTING

<110> Reed, John C.
Pio, Frederick F.
Godzik, Adam
Stehlik, Christian
Damiano, Jason S.
Lee, Sug-Hyung
Oliveira, Vasco A.
Hayashi, Hideki
Pawlowski, Krzysztof

<120> Novel Card Domain Containing
Polypeptides, Encoding Nucleic Acids, and Methods of Use

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Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu	
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TC250" P. 3542360

Trp	Met	Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly
465					470				475						480
Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe
			485						490						495
Leu	Leu	His	Ala	Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro
			500					505					510		
Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu
			515				520					525			
Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln
		530				535					540				
Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu
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 <211> 1107
 <212> DNA
 <213> Homo sapien

<400> 84
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 aaaaagtgtc ttgaaatcct tcaacatgat cctgattcta tcttagacac gttaacttct 180
 cggaggctga tttctgagga agagtatgag actctggaga atgttacaga tctcctgaag 240
 aaaagtcgga agctgttaat tttggtacag aaaaagggag aggcgacctg tcagcatttt 300
 ctcaagtgtt tatttagtac ttttccacag tcagctgcca tttgcggctt aaggcatgaa 360
 gttttaaaac atgagaatac agtacctcct caatctatgg gggcaagcag taattcagaa 420
 gatgcttttt ctctggaat aaaacagcct gaagcccctg agatcacagt gttcttcagt 480
 gagaaggaac acttggaatt ggaaacctct gagtttttca gggacaagaa aactagttat 540
 agggaaacag ctttgtctgc caggaagaat gagaaggaat atgacacacc agaagtcaca 600
 ttatcatatt cagttagaa agttggatgt gaagttccag caactattac atatataaaa 660
 gatggacaga gatatgagga gctagatgat tctttatact taggaaaaga ggaatatcta 720
 ggatctgttg acaccctga agatgcagaa gccactgtgg aagaggaggt ttatgatgac 780
 ccagagcacg ttggatatga tggatgaagag gacttcgaga attcagaaac cacagagttc 840
 tctggtgaag aaccaagtta tgagggatca gaaaccagcc tttcattgga ggaggaacag 900
 gagaaaagta tagaaggctg gtctcgaact catgggctta agcgatcctc ccacgttggc 960
 ctcccaaagt gctgggatta caggcgtgag ccaccctgcc tggcctgaaa attctgcctc 1020
 aaacatctca aacatccatt tatattttgt acaagaaagt aaataaaatt tttcttttta 1080
 acattaaaaa aaaaaaaaaa aaaaaaa 1107

<210> 85
 <211> 510
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (15)...(305)

<400> 85
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 Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu
 1 5 10

$$\begin{array}{ll} \langle 210 \rangle & 87 \\ \langle 211 \rangle & 97 \end{array}$$

<213> Homo sapien

[illegible]
$$\begin{array}{r} \langle 400 \rangle \quad 88 \\ 000 \end{array}$$

<213> Homo sapien

<222> (1) ... (318)

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1				5					10					15		
ggt	aca	ata	aat	ggc	tta	ctg	gat	gaa	tta	ttg	gag	aca	aat	gtg	ctg	96
Gly	Thr	Ile	Asn	Gly	Leu	Leu	Asp	Glu	Leu	Leu	Glu	Thr	Asn	Val	Leu	
			20					25					30			
agc	cag	gaa	gac	aca	gag	ata	gta	aaa	tgt	gaa	aat	gtt	aca	gtt	atc	144
Ser	Gln	Glu	Asp	Thr	Glu	Ile	Val	Lys	Cys	Glu	Asn	Val	Thr	Val	Ile	
		35					40					45				
gat	aag	gcc	cga	gat	ttg	ctt	gac	tct	gtt	att	cgg	aaa	ggg	gca	ggg	192
Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp	Ser	Val	Ile	Arg	Lys	Gly	Ala	Gly	
	50					55					60					
gca	tgt	gaa	att	tgc	atc	aca	tac	att	tgt	gaa	gaa	gac	agg	tac	ctg	240
Ala	Cys	Glu	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	Arg	Tyr	Leu	

att tgc tca ccg ccc aga gca caa gac ctc tga 321
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu
100 105

<400> 90															
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Gly	Thr	Ile	Asn	Gly	Leu	Leu	Asp	Glu	Leu	Leu	Glu	Thr	Asn	Val	Leu
			20					25					30		
Ser	Gln	Glu	Asp	Thr	Glu	Ile	Val	Lys	Cys	Glu	Asn	Val	Thr	Val	Ile
		35					40					45			
Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp	Ser	Val	Ile	Arg	Lys	Gly	Ala	Gly
	50					55				60					
Ala	Cys	Glu	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	Arg	Tyr	Leu
65					70					75					80
Ala	Gly	Thr	Leu	Gly	Leu	Ser	Ala	Gly	Asn	Asp	Tyr	Arg	Ala	Gly	Gly
				85					90					95	
Ile	Cys	Ser	Pro	Pro	Arg	Ala	Gln	Asp	Leu						
			100					105							

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<210> 91
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<212> PRT
<213> Homo sapien
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<400> 91																
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			20					25					30			
Asn	Val	Leu	Ser	Gln	Glu	Asp	Glu	Ile	Val	Lys	Arg	Glu	Asn	Ala	Thr	
		35					40					45				
Val	Ile	Asp	Lys	Ala	Arg	Ala	Leu	Leu	Asp	Ser	Val	Ile	Arg	Lys	Gly	
	50					55					60					
Ala	Gly	Ala	Cys	Glu	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	Ser	
65					70					75					80	
Tyr	Leu	Ala	Gly	Thr	Leu	Gly	Leu	Ser	Ala	Gly	Asn	Ala	Val	Gln	Ala	
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Gly	Gly	Ala	Cys	Ser	Thr	Ser	Ser	Gly	Gln	Asp	Leu					
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<400> 92
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<400> 93
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<400> 94
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<400> 95
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<212> DNA
<213> Homo sapien
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acatctgctg gaagtccctt gggattcaag gtacaggga tgaagagtag ttttacagaa 180
aaaagaggac aatatgggga tcaccttgga cttttccatt tggaaataat attttctatt 240
gtgttataga aagggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
                Met Asn Phe Ile Lys Asp
                        1                      5
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aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486

Ile 55	His	Met	Ile	Leu	Lys 60	Lys	Gly	Ser	Glu	Ser 65	Cys	Asn	Leu	Phe	Leu 70	
aaa Lys	tcc Ser	ctt Leu	aag Lys	gag Glu	tgg Trp	aac Asn	tat Tyr	cct Pro	cta Leu	ttt Phe	cag Gln	gac Asp	ttg Leu	aat Asn	gga Gly	534
				75					80					85		
caa Gln	agt Ser	ctt Leu	ttt Phe	cat His	cag Gln	aca Thr	tca Ser	gaa Glu	gga Gly	gac Asp	ttg Leu	gac Asp	gat Asp	ttg Leu	gct Ala	582
			90					95					100			
cag Gln	gat Asp	tta Leu	aag Lys	gac Asp	ttg Leu	tac Tyr	cat His	acc Thr	cca Pro	tct Ser	ttt Phe	ctg Leu	aac Asn	ttt Phe	tat Tyr	630
		105					110					115				
ccc Pro	ctt Leu	ggt Gly	gaa Glu	gat Asp	att Ile	gac Asp	att Ile	att Ile	ttt Phe	aac Asn	ttg Leu	aaa Lys	agc Ser	acc Thr	ttc Phe	678
	120					125				130						
aca Thr 135	gaa Glu	cct Pro	atc Ile	ctg Leu	tgg Trp	agg Arg	aag Lys	gac Asp	caa Gln	cac His	cat His	cac His	cgc Arg	gtg Val	gag Glu 150	726
					140					145						
cag Gln	ctg Leu	acc Thr	ctg Leu	aat Asn	ggc Gly	ctc Leu	ctg Leu	cag Gln	gct Ala	ctt Leu	cag Gln	agc Ser	ccc Pro	tgc Cys	atc Ile	774
				155					160					165		
att Ile	gaa Glu	ggg Gly	gaa Glu	tct Ser	ggc Gly	aaa Lys	ggc Gly	aag Lys	tcc Ser	act Thr	ctg Leu	ctg Leu	cag Gln	cgc Arg	att Ile	822
			170					175					180			
gcc Ala	atg Met	ctc Leu	tgg Trp	ggc Gly	tcc Ser	gga Gly	aag Lys	tgc Cys	aag Lys	gct Ala	ctg Leu	acc Thr	aag Lys	ttc Phe	aaa Lys	870
		185					190					195				
ttc Phe	gtc Val	ttc Phe	ttc Phe	ctc Leu	cgt Arg	ctc Leu	agc Ser	agg Arg	gcc Ala	cag Gln	ggt Gly	gga Gly	ctt Leu	ttt Phe	gaa Glu	918
	200					205					210					
acc Thr 215	ctc Leu	tgt Cys	gat Asp	caa Gln	ctc Leu	ctg Leu	gat Asp	ata Ile	cct Pro	ggc Gly	aca Thr	atc Ile	agg Arg	aag Lys	cag Gln 230	966
					220					225						
aca Thr	ttc Phe	atg Met	gcc Ala	atg Met	ctg Leu	ctg Leu	aag Lys	ctg Leu	cgg Arg	cag Gln	agg Arg	ggt Val	ctt Leu	ttc Phe	ctt Leu	1014
				235					240					245		
ctt Leu	gat Asp	ggc Gly	tac Tyr	aat Asn	gaa Glu	ttc Phe	aag Lys	ccc Pro	cag Gln	aac Asn	tgc Cys	cca Pro	gaa Glu	atc Ile	gaa Glu	1062
			250					255					260			
gcc Ala	ctg Leu	ata Ile	aag Lys	gaa Glu	aac Asn	cac His	cgc Arg	ttc Phe	aag Lys	aac Asn	atg Met	gtc Val	atc Ile	gtc Val	acc Thr	1110

	265					270					275							
act	acc	act	gag	tgc	ctg	agg	cac	ata	cgg	cag	ttt	ggt	gcc	ctg	act	1158		
Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg	Gln	Phe	Gly	Ala	Leu	Thr			
	280					285					290							
gct	gag	gtg	ggg	gat	atg	aca	gaa	gac	agc	gcc	cag	gct	ctc	atc	cga	1206		
Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser	Ala	Gln	Ala	Leu	Ile	Arg			
295					300					305						310		
gaa	gtg	ctg	atc	aag	gag	ctt	gct	gaa	ggc	ttg	ttg	ctc	caa	att	cag	1254		
Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly	Leu	Leu	Leu	Gln	Ile	Gln			
				315					320						325			
aaa	tcc	agg	tgc	ttg	agg	aat	ctc	atg	aag	acc	cct	ctc	ttt	gtg	gtc	1302		
Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys	Thr	Pro	Leu	Phe	Val	Val			
			330					335						340				
atc	act	tgt	gca	atc	cag	atg	ggt	gaa	agt	gag	ttc	cac	tct	cac	aca	1350		
Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser	Glu	Phe	His	Ser	His	Thr			
		345					350						355					
caa	aca	acg	ctg	ttc	cat	acc	ttc	tat	gat	ctg	ttg	ata	cag	aaa	aac	1398		
Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp	Leu	Leu	Ile	Gln	Lys	Asn			
	360					365					370							
aaa	cac	aaa	cat	aaa	ggt	gtg	gct	gca	agt	gac	ttc	att	cgg	agc	ctg	1446		
Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser	Asp	Phe	Ile	Arg	Ser	Leu			
375					380					385						390		
gac	cac	cgt	gga	gac	cta	gct	ctg	gag	ggt	gtg	ttc	tcc	cac	aag	ttt	1494		
Asp	His	Arg	Gly	Asp	Leu	Ala	Leu	Glu	Gly	Val	Phe	Ser	His	Lys	Phe			
				395					400						405			
gat	ttc	gaa	ctg	cag	gat	gtg	tcc	agc	gtg	aat	gag	gat	gtc	ctg	ctg	1542		
Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val	Asn	Glu	Asp	Val	Leu	Leu			
			410					415						420				
aca	act	ggg	ctc	ctc	tgt	aaa	tat	aca	gct	caa	agg	ttc	aag	cca	aag	1590		
Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala	Gln	Arg	Phe	Lys	Pro	Lys			
		425					430						435					
tat	aaa	ttc	ttt	cac	aag	tca	ttc	cag	gag	tac	aca	gca	gga	cga	aga	1638		
Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu	Tyr	Thr	Ala	Gly	Arg	Arg			
	440					445					450							
ctc	agc	agt	tta	ttg	acg	tct	cat	gag	cca	gag	gag	gtg	acc	aag	ggg	1686		
Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro	Glu	Glu	Val	Thr	Lys	Gly			
455					460					465						470		
aat	ggt	tac	ttg	cag	aaa	atg	gtt	tcc	att	tcg	gac	att	aca	tcc	act	1734		
Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile	Ser	Asp	Ile	Thr	Ser	Thr			
				475					480						485			

tat	agc	agc	ctg	ctc	cgg	tac	acc	tgt	ggg	tca	tct	gtg	gaa	gcc	acc	1782
Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	Glu	Ala	Thr	
			490						495			500				
agg	gct	gtt	atg	aag	cac	ctc	gca	gca	gtg	tat	caa	cac	ggc	tgc	ctt	1830
Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val	Tyr	Gln	His	Gly	Cys	Leu	
			505						510			515				
ctc	gga	ctt	tcc	atc	gcc	aag	agg	cct	ctc	tgg	aga	cag	gaa	tct	ttg	1878
Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	Trp	Arg	Gln	Glu	Ser	Leu	
			520						525			530				
caa	agt	gtg	aaa	aac	acc	act	gag	caa	gaa	att	ctg	aaa	gcc	ata	aac	1926
Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	Ile	Leu	Lys	Ala	Ile	Asn	
535						540						545			550	
atc	aat	tcc	ttt	gta	gag	tgt	ggc	atc	cat	tta	tat	caa	gag	agt	aca	1974
Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	Leu	Tyr	Gln	Glu	Ser	Thr	
			555						560						565	
tcc	aaa	tca	gcc	ctg	agc	caa	gaa	ttt	gaa	gct	ttc	ttt	caa	ggg	aaa	2022
Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	Ala	Phe	Phe	Gln	Gly	Lys	
			570						575						580	
agc	tta	tat	atc	aac	tca	ggg	aac	atc	ccc	gat	tac	tta	ttt	gac	ttc	2070
Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	Asp	Tyr	Leu	Phe	Asp	Phe	
			585						590						595	
ttt	gaa	cat	ttg	ccc	aat	tgt	gca	agt	gcc	ctg	gac	ttc	att	aaa	ctg	2118
Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	Leu	Asp	Phe	Ile	Lys	Leu	
			600						605						610	
gac	ttt	tat	ggg	gga	gct	atg	gct	tca	tgg	gaa	aag	gct	gca	gaa	gac	2166
Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp	Glu	Lys	Ala	Ala	Glu	Asp	
615						620						625			630	
aca	ggg	gga	atc	cac	atg	gaa	gag	gcc	cca	gaa	acc	tac	att	ccc	agc	2214
Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro	Glu	Thr	Tyr	Ile	Pro	Ser	
			635						640						645	
agg	gct	gta	tct	ttg	ttc	ttc	aac	tgg	aag	cag	gaa	ttc	agg	act	ctg	2262
Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	Gln	Glu	Phe	Arg	Thr	Leu	
			650						655						660	
gag	gtc	aca	ctc	cgg	gat	ttc	agc	aag	ttg	aat	aag	caa	gat	atc	aga	2310
Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	Asn	Lys	Gln	Asp	Ile	Arg	
			665						670						675	
tat	ctg	ggg	aaa	ata	ttc	agc	tct	gcc	aca	agc	ctc	agg	ctg	caa	ata	2358
Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	Ser	Leu	Arg	Leu	Gln	Ile	
			680						685						690	

aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc	2406
Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr	
695 700 705 710	
tggt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata	2454
Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile	
715 720 725	
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt	2502
Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser	
730 735 740	
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc	2550
Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser	
745 750 755	
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag	2598
Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys	
760 765 770	
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg	2646
Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu	
775 780 785 790	
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag	2694
Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu	
795 800 805	
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt	2742
Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu	
810 815 820	
gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa	2790
Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys	
825 830 835	
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat	2838
Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp	
840 845 850	
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa	2886
Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu	
855 860 865 870	
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg	2934
Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu	
875 880 885	
ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat	2982
Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His	
890 895 900	
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga	3030

Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg
905 910 915

ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac 3078
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn
920 925 930

cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc 3126
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser
935 940 945 950

agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa 3174
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln
955 960 965

tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca 3222
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala
970 975 980

tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa 3270
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln
985 990 995

gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt 3318
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val
1000 1005 1010

att aca ggt gct ttt aaa cta gta act gct taaataaagt gtactcgaag 3368
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala
1015 1020

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<210> 97
<211> 1024
<212> PRT
<213> Homo sapien

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Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
85 90 95
Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
100 105 110

CCDS: C34545.1

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	130					135					140				
His	His	His	Arg	Val	Glu	Gln	Leu	Thr	Leu	Asn	Gly	Leu	Leu	Gln	Ala
145					150					155					160
Leu	Gln	Ser	Pro	Cys	Ile	Ile	Glu	Gly	Glu	Ser	Gly	Lys	Gly	Lys	Ser
				165					170					175	
Thr	Leu	Leu	Gln	Arg	Ile	Ala	Met	Leu	Trp	Gly	Ser	Gly	Lys	Cys	Lys
			180					185					190		
Ala	Leu	Thr	Lys	Phe	Lys	Phe	Val	Phe	Phe	Leu	Arg	Leu	Ser	Arg	Ala
	195						200					205			
Gln	Gly	Gly	Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro
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Gly	Thr	Ile	Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg
225					230					235					240
Gln	Arg	Val	Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln
				245					250					255	
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			260					265					270		
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Gln	Phe	Gly	Ala	Leu	Thr	Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser
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Ala	Gln	Ala	Leu	Ile	Arg	Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly
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Leu	Leu	Leu	Gln	Ile	Gln	Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys
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Thr	Pro	Leu	Phe	Val	Val	Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser
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Glu	Phe	His	Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp
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	370					375					380				
Asp	Phe	Ile	Arg	Ser	Leu	Asp	His	Arg	Gly	Asp	Leu	Ala	Leu	Glu	Gly
385					390					395					400
Val	Phe	Ser	His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val
				405					410					415	
Asn	Glu	Asp	Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala
			420					425					430		
Gln	Arg	Phe	Lys	Pro	Lys	Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu
	435						440					445			
Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro
	450					455					460				
Glu	Glu	Val	Thr	Lys	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile
465					470					475					480
Ser	Asp	Ile	Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly
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Ser	Ser	Val	Glu	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val
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Tyr	Gln	His	Gly	Cys	Leu	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu
	515						520					525			
Trp	Arg	Gln	Glu	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu

530					535					540						
Ile	Leu	Lys	Ala	Ile	Asn	Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	
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Leu	Tyr	Gln	Glu	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	
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Ala	Phe	Phe	Gln	Gly	Lys	Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	
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Glu	Thr	Tyr	Ile	Pro	Ser	Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	
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Gln	Glu	Phe	Arg	Thr	Leu	Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	
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Asn	Lys	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	
675					680					685						
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Ser	Leu	Val	Leu	Ser	Thr	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu	
705					710					715					720	
Ala	Ser	Pro	Leu	Thr	Ile	Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr	
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Gly	Gly	Leu	Thr	Asp	Ser	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	
755					760					765						
Ile	Met	Asp	Asn	Ile	Lys	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	
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Glu	Gly	Leu	Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His	
785					790					795					800	
Leu	Ser	Asp	Ile	Gly	Glu	Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu	Ser	
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Ser	Glu	Pro	Cys	Asp	Leu	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys	Leu	
820					825					830						
Ser	Ala	Asn	Ala	Val	Lys	Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu	Val	
835					840					845						
Lys	Leu	Ser	Ile	Leu	Asp	Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp	Gly	
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Asn	Glu	Ala	Leu	His	Glu	Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu	Gln	
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Leu	Thr	Ala	Leu	Met	Leu	Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser	Leu	
885					890					895						
Ser	Ser	Leu	Leu	Lys	His	Leu	Glu	Glu	Val	Pro	Gln	Leu	Val	Lys	Leu	
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Gly	Leu	Lys	Asn	Trp	Arg	Leu	Thr	Asp	Thr	Glu	Ile	Arg	Ile	Leu	Gly	
915					920					925						
Ala	Phe	Phe	Gly	Lys	Asn	Pro	Leu	Lys	Asn	Phe	Gln	Gln	Leu	Asn	Leu	
930					935					940						
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<212> DNA
<213> Homo sapien
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<222> (277) ... (1353)
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acatctgctg	gaagtccctc	gggattcaag	gtacagggaa	tgaagagtag	ttttacagaa	180										
aaaagaggac	aatattggga	tcacctttga	cctttccatt	tggaaataat	attttctatt	240										
gtgttataga	aaggtgggaa	gctttcatcc	agaaca atg	aat ttc ata	aag gac	294										
			Met	Asn Phe Ile	Lys Asp											
			1		5											
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa						342										
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln																
	10		15		20											
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta						390										
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val																
	25		30		35											
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc						438										
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile																
	40		45		50											
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt						486										
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu																
55		60		65	70											
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga						534										
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly																
	75		80		85											
caa agt ggt ctg act gac agc ttg ggt aac ttg aag aac ctt aca aag						582										
Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys																
	90		95		100											
ctc ata atg gat aac ata aag atg aat gaa gaa gat gct ata aaa cta						630										

Leu	Ile	Met	Asp	Asn	Ile	Lys	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu		
105						110						115					
gct	gaa	ggc	ctg	aaa	aac	ctg	aag	aag	atg	tgt	tta	ttt	cat	ttg	acc	678	
Ala	Glu	Gly	Leu	Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr		
120						125						130					
cac	ttg	tct	gac	att	gga	gag	gga	atg	gat	tac	ata	gtc	aag	tct	ctg	726	
His	Leu	Ser	Asp	Ile	Gly	Glu	Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu		
135						140						145			150		
tca	agt	gaa	ccc	tgt	gac	ctt	gaa	gaa	att	caa	tta	gtc	tcc	tgc	tgc	774	
Ser	Ser	Glu	Pro	Cys	Asp	Leu	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys		
			155						160						165		
ttg	tct	gca	aat	gca	gtg	aaa	atc	cta	gct	cag	aat	ctt	cac	aat	ttg	822	
Leu	Ser	Ala	Asn	Ala	Val	Lys	Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu		
			170						175						180		
gtc	aaa	ctg	agc	att	ctt	gat	tta	tca	gaa	aat	tac	ctg	gaa	aaa	gat	870	
Val	Lys	Leu	Ser	Ile	Leu	Asp	Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp		
185						190						195					
gga	aat	gaa	gct	ctt	cat	gaa	ctg	atc	gac	agg	atg	aac	gtg	cta	gaa	918	
Gly	Asn	Glu	Ala	Leu	His	Glu	Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu		
200						205						210					
cag	ctc	acc	gca	ctg	atg	ctg	ccc	tgg	ggc	tgt	gac	gtg	caa	ggc	agc	966	
Gln	Leu	Thr	Ala	Leu	Met	Leu	Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser		
215						220						225			230		
ctg	agc	agc	ctg	ttg	aaa	cat	ttg	gag	gag	gtc	cca	caa	ctc	gtc	aag	1014	
Leu	Ser	Ser	Leu	Leu	Lys	His	Leu	Glu	Glu	Val	Pro	Gln	Leu	Val	Lys		
			235						240						245		
ctt	ggg	ttg	aaa	aac	tgg	aga	ctc	aca	gat	aca	gag	att	aga	att	tta	1062	
Leu	Gly	Leu	Lys	Asn	Trp	Arg	Leu	Thr	Asp	Thr	Glu	Ile	Arg	Ile	Leu		
			250						255						260		
ggc	gca	ttt	ttt	gga	aag	aac	cct	ctg	aaa	aac	ttc	cag	cag	ttg	aat	1110	
Gly	Ala	Phe	Phe	Gly	Lys	Asn	Pro	Leu	Lys	Asn	Phe	Gln	Gln	Leu	Asn		
265						270						275					
ttg	gcg	gga	aat	cgt	gtg	agc	agt	gat	gga	tgg	ctt	gcc	ttc	atg	ggc	1158	
Leu	Ala	Gly	Asn	Arg	Val	Ser	Ser	Asp	Gly	Trp	Leu	Ala	Phe	Met	Gly		
280						285						290					
gta	ttt	gag	aat	ctt	aag	caa	tta	gtg	ttt	ttt	gac	ttt	agt	act	aaa	1206	
Val	Phe	Glu	Asn	Leu	Lys	Gln	Leu	Val	Phe	Phe	Asp	Phe	Ser	Thr	Lys		
295						300						305			310		
gaa	ttt	cta	cct	gat	cca	gca	tta	gtc	aga	aaa	ctt	agc	caa	gtg	tta	1254	
Glu	Phe	Leu	Pro	Asp	Pro	Ala	Leu	Val	Arg	Lys	Leu	Ser	Gln	Val	Leu		

315

320

325

tcc aag tta act ttt ctg caa gaa gct agg ctt gtt ggg tgg caa ttt 1302
Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe
330 335 340

gat gat gat gat ctc agt gtt att aca ggt gct ttt aaa cta gta act 1350
Asp Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr
345 350 355

gct taaataaagt gtactcgaag caaaaaaaaaa aaaaaaaaaa aa 1395
Ala

<210> 99

<211> 359

<212> PRT

<213> Homo sapien

<400> 99

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Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn
85 90 95
Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu
100 105 110
Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met
115 120 125
Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly Met Asp
130 135 140
Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile
145 150 155 160
Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala
165 170 175
Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu
180 185 190
Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp
195 200 205
Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly
210 215 220
Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu
225 230 235 240
Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp
245 250 255

TC224230

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<210> 100
<211> 578
<212> DNA
<213> Homo sapien
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aaaactggtg atctgtttgc cctgtgtgac cttgccaga accctgctga ctgagagAAC 120
acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180
aaaagaggac aatattggga tcaccttga cctttccatt tggaaataat attttctatt 240
gtgttataga aaggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

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aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

578

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Met	Thr	Val	Ile	Lys	Gln	Ile	Thr	Asp	Asp	Leu	Phe	Val	Trp	Asn	Val
			20					25					30		
Leu	Asn	Arg	Glu	Glu	Val	Asn	Ile	Ile	Cys	Cys	Glu	Lys	Val	Glu	Gln
		35					40					45			
Asp	Ala	Ala	Arg	Gly	Ile	Ile	His	Met	Ile	Leu	Lys	Lys	Gly	Ser	Glu
	50					55					60				
Ser	Cys	Asn	Leu	Phe	Leu	Lys	Ser	Leu	Lys	Glu	Trp	Asn	Tyr	Pro	Leu
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Phe	Gln	Asp	Leu	Asn	Gly	Gln	Ser	Leu	Leu	Thr	Ala				
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<222> (277) ... (744)
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acatctgctg gaagtcctct gggattcaag gtacaggga tgaagagtag ttttacagaa 180
aaaagaggac aatattggga tcaccttga cctttccatt tggaaataat attttctatt 240
gtgttataga aaggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
                               Met Asn Phe Ile Lys Asp
                               1                               5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
          10                      15                      20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
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aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438

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Met	Thr	Val	Ile	Lys	Gln	Ile	Thr	Asp	Asp	Leu	Phe	Val	Trp	Asn	Val
			20					25					30		
Leu	Asn	Arg	Glu	Glu	Val	Asn	Ile	Ile	Cys	Cys	Glu	Lys	Val	Glu	Gln
		35					40					45			
Asp	Ala	Ala	Arg	Gly	Ile	Ile	His	Met	Ile	Leu	Lys	Lys	Gly	Ser	Glu
	50					55					60				
Ser	Cys	Asn	Leu	Phe	Leu	Lys	Ser	Leu	Lys	Glu	Trp	Asn	Tyr	Pro	Leu
65					70					75					80
Phe	Gln	Asp	Leu	Asn	Gly	Gln	Ser	Leu	Phe	His	Gln	Thr	Ser	Glu	Gly
				85					90					95	
Asp	Leu	Asp	Asp	Leu	Ala	Gln	Asp	Leu	Lys	Asp	Leu	Tyr	His	Thr	Pro
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Ser	Phe	Leu	Asn	Phe	Tyr	Pro	Leu	Gly	Glu	Asp	Ile	Asp	Ile	Ile	Phe

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<400> 107
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
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Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
                35                      40                      45
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu

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50	55	60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala		
65	70	75
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly		80
	85	90
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His		95
	100	105
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu		110
	115	120
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu		125
	130	135
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu		140
145	150	155
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln		160
	165	170
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala		175
	180	185
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln		190
	195	200
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu		205
	210	215
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met		220
225	230	235
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu		240
	245	250
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val		255
	260	265
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His		270
	275	280
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe		285
	290	295
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val		300
305	310	315
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu		320
	325	330
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr		335
	340	345
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg		350
	355	360
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn		365
	370	375
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser		380
385	390	395
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu		400
	405	410
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg		415
	420	425
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu		430
	435	440
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser		445
	450	455
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly		460
465	470	475
		480

FOE350 "F0043350"

Ser	Pro	Lys	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	
				485				490					495		
Leu	Leu	His	Ala	Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro
			500					505					510		
Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu
		515					520					525			
Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln
		530				535					540				
Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu
545					550					555					560
Val	Arg	Ala	Lys	Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe
				565					570					575	
Leu	His	Ile	Thr	Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu
			580					585					590		
Ser	Ala	Asp	Val	Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly
		595					600					605			
Arg	Pro	Gly	Asn	Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile
	610					615					620				
Gln	Ala	Ser	Glu	Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys
625					630					635					640
Ala	Glu	Pro	His	Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu
				645					650					655	
Leu	Ser	Arg	Glu	His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu
			660					665					670		
Lys	Ala	Leu	Leu	Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg
		675					680					685			
Ser	Leu	Arg	Lys	His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu
	690					695					700				
Ala	Lys	Ser	Val	His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser
705					710					715					720
Leu	Tyr	Glu	Met	Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly
				725					730					735	
Leu	Asn	Val	Gly	His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr
			740					745					750		
Glu	Cys	Ala	Ala	Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val
		755					760					765			
Ala	Leu	Gln	Leu	Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln
	770					775					780				
Leu	Leu	Pro	Cys	Leu	Gly	Val	Cys	Lys	Ala	Leu	Tyr	Leu	Arg	Asp	Asn
785				790						795					800
Asn	Ile	Ser	Asp	Arg	Gly	Ile	Cys	Lys	Leu	Ile	Glu	Cys	Ala	Leu	His
			805						810					815	
Cys	Glu	Gln	Leu	Gln	Lys	Leu	Ala	Leu	Gly	Asn	Asn	Tyr	Ile	Thr	Ala
			820					825					830		

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<210> 109

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$\langle 210 \rangle$ 110

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$\langle 210 \rangle$ 111

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<210> 112

<220>

<221> VARIANT

 $\langle 222 \rangle \quad (1) \dots (87)$

<223> Xaa = Any Amino Acid

$$\begin{array}{r} \langle 400 \rangle \quad 112 \\ 000 \end{array}$$

<210> 113

$$\begin{matrix} <400> & 113 \\ & 000 \end{matrix}$$

<210> 114

[illegible]

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For the purpose of the present study

<210> 125

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<210> 127

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 145

ccagaattca tggccgacaa ggtcctgaag

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<210> 146

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<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 146

ccactcgagc taatttccag gtatcggacc

30

<210> 147

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 147

gaagacagtt acctggcaga

20

<210> 148

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 148

ttgtattctg aacatggcac c

21

<210> 149

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 149

gatcatcatc caggccgccc gtggtgacag ccctgg

36

<210> 150

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 150

ccagggctgt caccacgggc ggcttgatg atgac

36

<210> 151

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 151

cggaattcat ggccgacaag gtcctg

26

<210> 152

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 152

cgctcgagtt agtcttgcatttccaga

38

<210> 153

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 153

catgtgaatg atccctctag cag

23

<210> 154

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 154

gggctcggct atcgtgctct a

21

<210> 155

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 155
acgatagccg agcccttatt c 21

<210> 156
<211> 21
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<400> 156
gtatggaatg ttctgaatcg c 21

<210> 157
<211> 33
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<220>
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<400> 157
cccgatcca tgaatttcat aaaggacaat agc 33

<210> 158
<211> 30
<212> DNA
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<220>
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<400> 158
cccttcgaac aagtcctgaa atagaggata 30

<210> 159
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<220>
<223> primer

<400> 159
ggtggagcag gatgctgcta gagg 24

Sequence

<210> 160
<211> 29
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cacagtggtc caggctccga atgaagtca 29

<210> 161
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<220>
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<400> 161
catcatttgc tgcgagaagg tggag 25

<210> 162
<211> 25
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<400> 162
ttaacttgga taacacttgg ctaag 25

<210> 163
<211> 23
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<220>
<223> primer

<400> 163
gtaaacatca ttgctgcga gaa 23

<210> 164
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

Patented Feb 23, 2000

<400> 164
cccgggcagg tagaagatgc tat 23

<210> 165
<211> 25
<212> DNA
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<220>
<223> primer

<400> 165
aatttcataa aggacaatag ccgag 25

<210> 166
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 166
tgtctactgt acttttctaag ctggt 25

<210> 167
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (225)

<400> 167
gag agt act ccc tca gag atc ata gaa aga gaa aga aaa aag ttg ctt 48
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
1 5 10 15

gaa atc ctt caa cat gat cct gat tct atc tta gac acg tta act tct 96
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
20 25 30

cgg agg ctg att tct gag gaa gag tat gag act ctg gag aat gtt aca 144
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
35 40 45

gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta cag aaa aag 192
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
50 55 60

gga gag gcg acc tgt cag cat ttt ctc aag tgt 225
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys

65

70

75

<210> 168

<211> 75

<212> PRT

<213> Homo sapiens

<400> 168

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Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
 1           5           10           15
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
          20           25           30
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
          35           40           45
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
          50           55           60
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys
65           70           75

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<210> 169

<211> 228

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (228)

<400> 169

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atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag      48
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
 1           5           10           15

ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg      96
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
          20           25           30

ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac      144
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
          35           40           45

ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc      192
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
          50           55           60

gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc                        228
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
65           70           75

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<210> 170

1254960

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<211> 76
<212> PRT
<213> Homo sapiens
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<400> 170															
Met	Cys	Ser	Gln	Glu	Ala	Phe	Gln	Ala	Gln	Arg	Ser	Gln	Leu	Val	Glu
1				5					10				15		
Leu	Leu	Val	Ser	Gly	Ser	Leu	Glu	Gly	Phe	Glu	Ser	Val	Leu	Asp	Trp
			20					25					30		
Leu	Leu	Ser	Trp	Glu	Val	Leu	Ser	Trp	Glu	Asp	Tyr	Glu	Gly	Phe	His
		35					40					45			
Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu	Asp	Thr
	50					55					60				
Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu				
65					70					75					

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<210> 171
<211> 243
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (243)
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<400> 171																	
cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg ctc	48																
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu																	
1 5 10 15																	
cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt ttc	96																
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe																	
20 25 30																	
gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca ccg	144																
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro																	
35 40 45																	
tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg aat	192																
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn																	
50 55 60																	
gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc cca	240																
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro																	
65 70 75 80																	
ttg	243																
Leu																	

<210> 172

<211> 81
<212> PRT
<213> Homo sapiens

<400> 172
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu
1 5 10 15
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe
20 25 30
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro
35 40 45
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn
50 55 60
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro
65 70 75 80
Leu

<210> 173
<211> 888
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (888)

<400> 173
gac gat gcg gac act gtg ctg gtg gtg ggt gag gcg ggc agt ggc aag 48
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
1 5 10 15
agc acg ctc ctg cag cgg ctg cac ttg ctg tgg gct gca ggg caa gac 96
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
20 25 30
ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg cag 144
Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
35 40 45
tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac tgc 192
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
50 55 60
tgt tgg cct gat gtt ggt caa gaa gac atc ttc cag tta ctc ctt gac 240
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp
65 70 75 80
cac cct gac cgt gtc ctg tta acc ttt gat ggc ttt gag gag ttc aag 288
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
85 90 95

TCGA 454566

ttc	agg	ttc	acg	gat	cgt	gaa	cgc	cac	tgc	tcc	ccg	acc	gac	ccc	acc		336
Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	His	Cys	Ser	Pro	Thr	Asp	Pro	Thr		
			100					105					110				
tct	gtc	cag	acc	ctg	ctc	ttc	aac	ctt	ctg	cag	ggc	aac	ctg	ctg	aag		384
Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn	Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys		
		115					120					125					
aat	gcc	cgc	aag	gtg	gtg	acc	agc	cgt	ccg	gcc	gct	gtg	tcg	gcg	ttc		432
Asn	Ala	Arg	Lys	Val	Val	Thr	Ser	Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe		
	130					135					140						
ctc	agg	aag	tac	atc	cgc	acc	gag	ttc	aac	ctc	aag	ggc	ttc	tct	gaa		480
Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu	Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu		
145					150					155					160		
cag	ggc	atc	gag	ctg	tac	ctg	agg	aag	cgc	cat	cat	gag	ccc	ggg	gtg		528
Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg	Lys	Arg	His	His	Glu	Pro	Gly	Val		
				165				170						175			
gcg	gac	cgc	ctc	atc	cgc	ctg	ctc	caa	gag	acc	tca	gcc	ctg	cac	ggc		576
Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Ala	Leu	His	Gly		
			180					185					190				
ttg	tgc	cac	ctg	cct	gtc	ttc	tca	tgg	atg	gtg	tcc	aaa	tgc	cac	cag		624
Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser	Lys	Cys	His	Gln		
		195					200					205					
gaa	ctg	ttg	ctg	cag	gag	ggg	ggg	tcc	cca	aag	acc	act	aca	gat	atg		672
Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met		
	210					215					220						
tac	ctg	ctg	att	ctg	cag	cat	ttt	ctg	ctg	cat	gcc	acc	ccc	cca	gac		720
Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala	Thr	Pro	Pro	Asp		
225					230					235					240		
tca	gct	tcc	caa	ggc	ctg	gga	ccc	agt	ctt	ctt	cgg	ggc	cgc	ctc	ccc		768
Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro		
				245				250						255			
acc	ctc	ctg	cac	ctg	ggc	aga	ctg	gct	ctg	tgg	ggc	ctg	ggc	atg	tgc		816
Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys		
			260					265					270				
tgc	tac	gtg	ttc	tca	gcc	cag	cag	ctc	cag	gca	gca	cag	gtc	agc	cct		864
Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro		
		275					280					285					
gat	gac	att	tct	ctt	ggc	ttc	ctg										888
Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu										
	290					295											

<210> 174
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 174
 Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
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 Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
 20 25 30
 Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
 35 40 45
 Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
 50 55 60
 Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp
 65 70 75 80
 His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
 85 90 95
 Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr
 100 105 110
 Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys
 115 120 125
 Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe
 130 135 140
 Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu
 145 150 155 160
 Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val
 165 170 175
 Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly
 180 185 190
 Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln
 195 200 205
 Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr Thr Thr Asp Met
 210 215 220
 Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp
 225 230 235 240
 Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro
 245 250 255
 Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys
 260 265 270
 Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro
 275 280 285
 Asp Asp Ile Ser Leu Gly Phe Leu
 290 295

<210> 175
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

174 296 175 1209 DNA

<400> 175

gag	ccc	ggg	gtg	gcg	gac	cgc	ctc	atc	cgc	ctg	ctc	caa	gag	acc	tca	48
Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu	Thr	Ser	
1				5					10					15		
gcc	ctg	cac	ggg	ttg	tgc	cac	ctg	cct	gtc	ttc	tca	tgg	atg	gtg	tcc	96
Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser	
			20					25					30			
aaa	tgc	cac	cag	gaa	ctg	ttg	ctg	cag	gag	ggg	ggg	tcc	cca	aag	acc	144
Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr	
		35					40					45				
act	aca	gat	atg	tac	ctg	ctg	att	ctg	cag	cat	ttt	ctg	ctg	cat	gcc	192
Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala	
	50					55					60					
acc	ccc	cca	gac	tca	gct	tcc	caa	ggg	ctg	gga	ccc	agt	ctt	ctt	cgg	240
Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg	
65				70				75							80	
ggc	cgc	ctc	ccc	acc	ctc	ctg	cac	ctg	ggc	aga	ctg	gct	ctg	tgg	ggc	288
Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly	
			85					90						95		
ctg	ggc	atg	tgc	tgc	tac	gtg	ttc	tca	gcc	cag	cag	ctc	cag	gca	gca	336
Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala	
			100					105					110			
cag	gtc	agc	cct	gat	gac	att	tct	ctt	ggc	ttc	ctg	gtg	cgt	gcc	aaa	384
Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu	Val	Arg	Ala	Lys	
		115					120					125				
ggg	gtc	gtg	cca	ggg	agt	acg	gcg	ccc	ctg	gaa	ttc	ctt	cac	atc	act	432
Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe	Leu	His	Ile	Thr	
	130					135					140					
ttc	cag	tgc	ttc	ttt	gcc	gcg	ttc	tac	ctg	gca	ctc	agt	gct	gat	gtg	480
Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu	Ser	Ala	Asp	Val	
145					150					155					160	
cca	cca	gct	ttg	ctc	aga	cac	ctc	ttc	aat	tgt	ggc	agg	cca	ggc	aac	528
Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly	Arg	Pro	Gly	Asn	
			165					170						175		
tca	cca	atg	gcc	agg	ctc	ctg	ccc	acg	atg	tgc	atc	cag	gcc	tcg	gag	576
Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile	Gln	Ala	Ser	Glu	
			180					185					190			
gga	aag	gac	agc	agc	gtg	gca	gct	ttg	ctg	cag	aag	gcc	gag	ccg	cac	624
Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys	Ala	Glu	Pro	His	

195	200	205	
aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg ttg tcc cgg gag			672
Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu			
210	215	220	
cac tgg ggc ctg ctg gct gag tgc cag aca tct gag aag gcc ctg ctc			720
His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu			
225	230	235	240
cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc cgc aag			768
Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys			
245	250	255	
cac ttc cac tcc atc ccg cca gct gca ccg ggt gag gcc aag agc gtg			816
His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val			
260	265	270	
cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc ctg tac gag atg			864
His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met			
275	280	285	
cag gag gag cgg ctg gct cgg aag gct gca cgt ggc ctg aat gtt ggg			912
Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly			
290	295	300	
cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act gag tgt gct gcc			960
His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala			
305	310	315	320
ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg gcc ctg cag ctg			1008
Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu			
325	330	335	
gac tac aac tct gtg ggt gac att ggc gtg gag cag ctg ctg cct tgc			1056
Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys			
340	345	350	
ctt ggt gtc tgc aag gct ctg tat ttg cgc gat aac aat atc tca gac			1104
Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp			
355	360	365	
cga ggc atc tgc aag ctc att gaa tgt gct ctt cac tgc gag caa ttg			1152
Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu			
370	375	380	
cag aag tta gcg ctg ggg aat aac tac atc act gcc gcg gga gcc caa			1200
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln			
385	390	395	400
gtg ctg gcc			1209
Val Leu Ala			

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

<400> 176																
Glu 1	Pro	Gly	Val	Ala 5	Asp	Arg	Leu	Ile	Arg 10	Leu	Leu	Gln	Glu	Thr 15	Ser	
Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser	
			20					25					30			
Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr	
		35					40					45				
Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala	
	50					55					60					
Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg	
65					70					75					80	
Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly	
				85					90					95		
Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala	
			100					105					110			
Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu	Val	Arg	Ala	Lys	
		115					120						125			
Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe	Leu	His	Ile	Thr	
	130					135					140					
Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu	Ser	Ala	Asp	Val	
145					150					155					160	
Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly	Arg	Pro	Gly	Asn	
				165					170					175		
Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile	Gln	Ala	Ser	Glu	
			180					185					190			
Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys	Ala	Glu	Pro	His	
		195				200						205				
Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu	Leu	Ser	Arg	Glu	
	210					215					220					
His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu	Lys	Ala	Leu	Leu	
225					230					235					240	
Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg	Ser	Leu	Arg	Lys	
				245					250					255		
His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu	Ala	Lys	Ser	Val	
			260					265					270			
His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser	Leu	Tyr	Glu	Met	
		275					280					285				
Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly	Leu	Asn	Val	Gly	
	290					295					300					
His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr	Glu	Cys	Ala	Ala	
305					310					315					320	
Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val	Ala	Leu	Gln	Leu	
				325					330					335		
Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln	Leu</				

355	360	365
Arg Gly Ile Cys Lys Leu	Ile Glu Cys Ala Leu	His Cys Glu Gln Leu
370	375	380
Gln Lys Leu Ala Leu Gly	Asn Asn Tyr Ile Thr	Ala Ala Gly Ala Gln
385	390	395
Val Leu Ala		400

<210> 177
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(261)

<400> 177

atg aat ttc ata aag gac aat agc cga gcc ctt att caa aga atg gga	48
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly	
1 5 10 15	
atg act gtt ata aag caa atc aca gat gac cta ttt gta tgg aat gtt	96
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val	
20 25 30	
ctg aat cgc gaa gaa gta aac atc att tgc tgc gag aag gtg gag cag	144
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln	
35 40 45	
gat gct gct aga ggg atc att cac atg att ttg aaa aag ggt tca gag	192
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu	
50 55 60	
tcc tgt aac ctc ttt ctt aaa tcc ctt aag gag tgg aac tat cct cta	240
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu	
65 70 75 80	
ttt cag gac ttg aat gga caa	261
Phe Gln Asp Leu Asn Gly Gln	
85	

<210> 178
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 178

Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val

TC6250 "TC6430"

	20		25		30										
Leu	Asn	Arg	Glu	Glu	Val	Asn	Ile	Ile	Cys	Cys	Glu	Lys	Val	Glu	Gln
	35					40					45				
Asp	Ala	Ala	Arg	Gly	Ile	Ile	His	Met	Ile	Leu	Lys	Lys	Gly	Ser	Glu
	50					55					60				
Ser	Cys	Asn	Leu	Phe	Leu	Lys	Ser	Leu	Lys	Glu	Trp	Asn	Tyr	Pro	Leu
65					70					75					80
Phe	Gln	Asp	Leu	Asn	Gly	Gln									
					85										

<210> 179
 <211> 891
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(891)

<400> 179

ctt	cag	agc	ccc	tgc	atc	att	gaa	ggg	gaa	tct	ggc	aaa	ggc	aag	tcc	48
Leu	Gln	Ser	Pro	Cys	Ile	Ile	Glu	Gly	Glu	Ser	Gly	Lys	Gly	Lys	Ser	
1				5					10					15		
act	ctg	ctg	cag	cgc	att	gcc	atg	ctc	tgg	ggc	tcc	gga	aag	tgc	aag	96
Thr	Leu	Leu	Gln	Arg	Ile	Ala	Met	Leu	Trp	Gly	Ser	Gly	Lys	Cys	Lys	
			20					25					30			
gct	ctg	acc	aag	ttc	aaa	ttc	gtc	ttc	ttc	ctc	cgt	ctc	agc	agg	gcc	144
Ala	Leu	Thr	Lys	Phe	Lys	Phe	Val	Phe	Phe	Leu	Arg	Leu	Ser	Arg	Ala	
		35					40					45				
cag	ggt	gga	ctt	ttt	gaa	acc	ctc	tgt	gat	caa	ctc	ctg	gat	ata	cct	192
Gln	Gly	Gly	Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro	
	50					55					60					
ggc	aca	atc	agg	aag	cag	aca	ttc	atg	gcc	atg	ctg	ctg	aag	ctg	cgg	240
Gly	Thr	Ile	Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg	
65					70				75						80	
cag	agg	gtt	ctt	ttc	ctt	ctt	gat	ggc	tac	aat	gaa	ttc	aag	ccc	cag	288
Gln	Arg	Val	Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln	
			85					90						95		
aac	tgc	cca	gaa	atc	gaa	gcc	ctg	ata	aag	gaa	aac	cac	cgc	ttc	aag	336
Asn	Cys	Pro	Glu	Ile	Glu	Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys	
		100						105					110			
aac	atg	gtc	atc	gtc	acc	act	acc	act	gag	tgc	ctg	agg	cac	ata	cgg	384
Asn	Met	Val	Ile	Val	Thr	Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg	
		115					120						125			

179 891 DNA Homo sapiens CDS (1)...(891)

cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc 432
 Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
 130 135 140

gcc cag gct ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc 480
 Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
 145 150 155 160

ttg ttg ctc caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag 528
 Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
 165 170 175

acc cct ctc ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt 576
 Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
 180 185 190

gag ttc cac tct cac aca caa aca acg ctg ttc cat acc ttc tat gat 624
 Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
 195 200 205

ctg ttg ata cag aaa aac aaa cac aaa cat aaa ggt gtg gct gca agt 672
 Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
 210 215 220

gac ttc att cgg agc ctg gac cac cgt gga gac cta gct ctg gag ggt 720
 Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
 225 230 235 240

gtg ttc tcc cac aag ttt gat ttc gaa ctg cag gat gtg tcc agc gtg 768
 Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
 245 250 255

aat gag gat gtc ctg ctg aca act ggg ctc ctc tgt aaa tat aca gct 816
 Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
 260 265 270

caa agg ttc aag cca aag tat aaa ttc ttt cac aag tca ttc cag gag 864
 Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
 275 280 285

tac aca gca gga cga aga ctc agc agt 891
 Tyr Thr Ala Gly Arg Arg Leu Ser Ser
 290 295

<210> 180
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 180
 Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
 1 5 10 15

CCDS: T23433.1

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Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
      20              25              30
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
      35              40              45
Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
      50              55              60
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
      65              70              75              80
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
      85              90              95
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
      100             105             110
Asn Met Val Ile Val Thr Thr Thr Thr Glu Cys Leu Arg His Ile Arg
      115             120             125
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
      130             135             140
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
      145             150             155             160
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
      165             170             175
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
      180             185             190
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
      195             200             205
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
      210             215             220
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
      225             230             235             240
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
      245             250             255
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
      260             265             270
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
      275             280             285
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
      290             295

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<210> 181
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(618)

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 Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
 1 5 10 15

aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg aag 96

126250 126250

Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys	
20 25 30	
aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag gga	144
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly	
35 40 45	
atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt gaa	192
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu	
50 55 60	
gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa atc	240
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile	
65 70 75 80	
cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat tta	288
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu	
85 90 95	
tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa ctg	336
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu	
100 105 110	
atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg ccc	384
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro	
115 120 125	
tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat ttg	432
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu	
130 135 140	
gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga ctc	480
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu	
145 150 155 160	
aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac cct	528
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro	
165 170 175	
ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc agt	576
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser	
180 185 190	
gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag	618
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys	
195 200 205	

<210> 182
 <211> 206
 <212> PRT
 <213> Homo sapiens

TC22607234360

<400> 182

Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
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 Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys
 20 25 30
 Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly
 35 40 45
 Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu
 50 55 60
 Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile
 65 70 75 80
 Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu
 85 90 95
 Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu
 100 105 110
 Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro
 115 120 125
 Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu
 130 135 140
 Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu
 145 150 155 160
 Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro
 165 170 175
 Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser
 180 185 190
 Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys
 195 200 205

<210> 183

<211> 165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(165)

<400> 183

acc tac att ccc agc agg gct gta tct ttg ttc ttc aac tgg aag cag 48
 Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
 1 5 10 15
 gaa ttc agg act ctg gag gtc aca ctc cgg gat ttc agc aag ttg aat 96
 Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
 20 25 30
 aag caa gat atc aga tat ctg ggg aaa ata ttc agc tct gcc aca agc 144
 Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
 35 40 45
 ctc agg ctg caa ata aag aga 165

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<210> 185
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 185
gaaatgtgct cgcaggagg
19

<210> 186
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 186
gatgagcttc tgacaggccc
20

<210> 187
<211> 3063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (2385)

<221> CDS
<222> (2389) ... (2928)

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Cys	Glu	Met	Cys	Ser	Gln	Glu	Ala	Phe	Gln	Ala	Gln	Arg	Ser	Gln	Leu		
1				5					10					15			
gtc	gag	ctg	ctg	gtc	tca	ggg	tcc	ctg	gaa	ggc	ttc	gag	agt	gtc	ctg		96
Val	Glu	Leu	Leu	Val	Ser	Gly	Ser	Leu	Glu	Gly	Phe	Glu	Ser	Val	Leu		
			20					25					30				
gac	tgg	ctg	ctg	tcc	tgg	gag	gtc	ctc	tcc	tgg	gag	gac	tac	gag	ggc		144
Asp	Trp	Leu	Leu	Ser	Trp	Glu	Val	Leu	Ser	Trp	Glu	Asp	Tyr	Glu	Gly		
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ttc	cac	ctc	ctg	ggc	cag	cct	ctc	tcc	cac	ttg	gcc	agg	cgc	ctt	ctg		192
Phe	His	Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu		
	50					55					60						
gac	acc	gtc	tgg	aat	aag	ggc	act	tgg	gcc	tgt	cag	aag	ctc	atc	gcg		240
Asp	Thr	Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu	Ile	Ala		
65					70					75					80		
gct	gcc	caa	gaa	gcc	cag	gcc	gac	agc	cag	tcc	ccc	aag	ctg	cat	ggc		288
Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly		
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tgc	tgg	gac	ccc	cac	tcg	ctc	cac	cca	gcc	cga	gac	ctg	cag	agt	cac		336
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His		
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cgg	cca	gcc	att	gtc	agg	agg	ctc	cac	agc	cat	gtg	gag	aac	atg	ctg		384
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu		
		115					120					125					
gac	ctg	gca	tgg	gag	cgg	ggc	ttc	gtc	agc	cag	tat	gaa	tgt	gat	gaa		432
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu		
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Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu		
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Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln		
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cat	gtt	cag	gaa	tta	cca	gtc	cca	ttg	gcc	ctg	cct	ttg	gaa	gct	gcc		576
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala		
			180					185					190				
aca	tgc	aag	aag	tat	atg	gcc	aag	ctg	agg	acc	acg	gtg	tct	gct	cag		624
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val					

tct cgc ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag 672
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu
210 215 220

gac ata tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg 720
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met
225 230 235 240

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Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu
245 250 255

ttc agc acc cct ggc cac ctc aat gac gat gcg gac act gtg ctg gtg 816
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val
260 265 270

gtg ggt gag gcg ggc agt ggc aag agc acg ctc ctg cag cgg ctg cac 864
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
275 280 285

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Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
290 295 300

cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg 960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320

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Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
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Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
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Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
355 360 365

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His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
370 375 380

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Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
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Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
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1248390-1248395

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Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu	
435 440 445	
caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca	1392
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser	
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tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg	1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly	
465 470 475 480	
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Ser Pro Lys Thr Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe	
485 490 495	
ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc	1536
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro	
500 505 510	
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Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu	
515 520 525	
gct ctg tgg ggc ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag	1632
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln	
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Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu	
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Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe	
565 570 575	
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Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu	
580 585 590	
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Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly	
595 600 605	
agg cca ggc aac tca cca atg gcc agg ctc ctg ccc acg atg tgc atc	1872
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile	
610 615 620	
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Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys	
625 630 635 640	
gcc gag ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg	1968
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu	
645 650 655	
ttg tcc cgg gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag	2016
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu	
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aag gcc ctg ctc cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc	2064
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg	
675 680 685	
agc ctc cgc aag cac ttc cac tcc atc ccg cca gct gca ccg ggt gag	2112
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu	
690 695 700	
gcc aag agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc	2160
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser	
705 710 715 720	
ctg tac gag atg cag gag gag cgg ctg gct cgg aag gct gca cgt ggc	2208
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly	
725 730 735	
ctg aat gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act	2256
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr	
740 745 750	
gag tgt gct gcc ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg	2304
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val	
755 760 765	
gcc ctg cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag	2352
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln	
770 775 780	
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Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Phe Trp Gly Asn	
785 790 795	
aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat	2448
Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp	
800 805 810 815	
cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt	2496
His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser	
820 825 830	
gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta	2544
Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu	

835	840	845	
gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt			2592
Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys			
850	855	860	
tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aac			2640
Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Asn			
865	870	875	
ata aaa att cat gct tgc gga ttc aac aaa ctc ttg gaa agc att ttc			2688
Ile Lys Ile His Ala Ser Gly Phe Asn Lys Leu Leu Glu Ser Ile Phe			
880	885	890	895
tgc atc ctc ctg gtt gtg gaa gca ttt ttc ctg cag aaa gtt gtc aag			2736
Cys Ile Leu Leu Val Val Glu Ala Phe Phe Leu Gln Lys Val Val Lys			
900	905	910	
att ctt gaa gaa atg gta gtc agt tgg cta gag gtc agg ttg tcc aat			2784
Ile Leu Glu Glu Met Val Val Ser Trp Leu Glu Val Arg Leu Ser Asn			
915	920	925	
aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa			2832
Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu			
930	935	940	
agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc tct			2880
Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe Ser			
945	950	955	
cta gag gag gtt gac aag ctc ggc tgc agg gac acc aga ctc ttg ctt			2928
Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr Arg Leu Leu Leu			
960	965	970	975
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Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly			
35 40 45			
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu			
50 55 60			
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala			

TC6250-164260

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Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly
				85					90					95	
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His
			100					105					110		
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu
		115					120					125			
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu
	130					135					140				
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu
145					150					155					160
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln
				165				170						175	
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala
			180					185					190		
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln
		195					200					205			
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu
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Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met
225					230				235						240
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu
				245					250					255	
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val
			260					265					270		
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His
	275						280					285			
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe
	290					295				300					
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val
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Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu
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Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr
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Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg
	355						360					365			
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn
	370					375					380				
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser
385					390					395					400
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu
				405					410					415	
Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg
		420						425					430		
Lys	Arg	His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu
		435					440						445		
Gln	Glu	Thr	Ser	Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser
	450					455					460				
Trp	Met	Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly
465					470					475					480
Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe
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FOE22490

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Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
    515                      520                      525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
    530                      535                      540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545                      550                      555                      560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
    565                      570                      575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
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Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
    595                      600                      605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
    610                      615                      620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625                      630                      635                      640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
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Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
    660                      665                      670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
    675                      680                      685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
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Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705                      710                      715                      720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
    725                      730                      735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
    740                      745                      750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
    755                      760                      765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
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ctgctgggaa ggctgctgcc caacctgtgt atccagggtc ccagagtcaa gaagggcagc 180
gaagcagccc tg ctg cag aag gct gag cca cac aac ctg caa atc aca gca 231
          Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala
          1              5              10

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gca tgc cag gtc tcc gag agg gta ctg ctc cag cgt cag gca cgt gcc 327
Ala Cys Gln Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala
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cgc tcg tgt ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg 375
Arg Ser Cys Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro
50 55 60

cct gcc gtg ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttc 423
Pro Ala Val Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe
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Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala
80 85 90

cag gag gct gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt 519
Gln Glu Ala Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe
95 100 105

tgc aga gtg ggc cct gca gag tgt gct gca ctg gcc ttt gta ctg caa 567
Cys Arg Val Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln
110 115 120 125

cat ctc cag cgg cct gtg gcc cta cag ctg gat tac aac tct gtg 612
His Leu Gln Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val
130 135 140

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Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
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Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu
65 70 75 80
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala
85 90 95
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
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Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
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<220>
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<222> (1)...(417)

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Ile Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
          35          40          45
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
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Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu

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Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala
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Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
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Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
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Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser
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